

screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO382 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO382 [herein designated as UNQ323 (DNA45234-1277)] (SEQ ID NO:68) and the derived protein sequence for PRO382.

The entire nucleotide sequence of UNQ323 (DNA45234-1277) is shown in Figure 27 (SEQ ID NO:68). Clone UNQ323 (DNA45234-1277) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 126-128 and ending at the stop codon at nucleotide positions 1485-1487 (Figure 27). The predicted polypeptide precursor is 453 amino acids long (Figure 28). The full-length PRO382 protein shown in Figure 28 has an estimated molecular weight of about 49,334 daltons and a pI of about 6.32. Analysis of the native PRO382 amino acid sequence shown in Figure 28 (SEQ ID NO:69) indicates the presence of a putative transmembrane domain from about amino acid 240 to about amino acid 284, a putative signal peptide at about amino acid 1 to about amino acid 20, a putative apple domain at about amino acid 386 to about amino acid 419, a putative Kringle domain at about amino acid 394 to about amino acid 406 and a histidine-containing protease active site at about amino acid 253 to about amino acid 258. Clone UNQ323 (DNA45234-1277) has been deposited with ATCC on March 5, 1998 and is assigned ATCC deposit no. 209654.

Analysis of the amino acid sequence of the full-length PRO382 polypeptide suggests that it possess significant homology to serine protease proteins, thereby indicating that PRO382 may be a novel serine protease. Specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO382 amino acid sequence and the following Dayhoff sequences, HSU75329_1, ENTK_MOUSE, HEPS_HUMAN, AF030065_1, HEPS_RAT, PLMN_PIG, P_R89430, P_R89435, PLMN_HORSE, PLMN_BOVIN and P_R83959.

EXAMPLE 13: Isolation of cDNA Clones Encoding Human PRO545

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA44706. An EST proprietary to Genentech was employed in the consensus assembly and is herein designated DNA13217 (Figure 31; SEQ ID NO:75). Based on the DNA44706 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO545.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-GTCTCAGCAGTGTTCTGGTCTCAGGG-3' (SEQ ID NO:76)

forward PCR primer 2 5'-CATGAGCATGTGCACGGC-3' (SEQ ID NO:77)

forward PCR primer 3 5'-TACCTGCACGATGGGCAC-3' (SEQ ID NO:78)

forward PCR primer 4 5'-CACTGGGCACCTCCCTTC-3' (SEQ ID NO:79)

reverse PCR primer 1 5'-CTCCAGGCTGGTCTCCAAGTCCTTCC-3' (SEQ ID NO:80)

reverse PCR primer 2 5'-TCCCTGTTGGACTCTGCAGCTTCC-3' (SEQ ID NO:81)

reverse PCR primer 3 5'-CTTCGCTGGGAAGAGTTTG-3' (SEQ ID NO:82)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA44706 sequence which had the following nucleotide sequence

hybridization probe

5'-GTGCAACCAACAGATACAAACTCTTCCAGCGAAGAAGCTGAAAAGCGTC-3'

(SEQ ID NO:83)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO545 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human placenta tissue (LIB90).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO545 [herein designated as UNQ346 (DNA49624-1279)] (SEQ ID NO:73) and the derived protein sequence for PRO545.

The entire nucleotide sequence of UNQ346 (DNA49624-1279) is shown in Figure 29 (SEQ ID NO:73). Clone UNQ346 (DNA49624-1279) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 311-313 and ending at the stop codon at nucleotide positions 2516-2518 (Figure 29). The predicted polypeptide precursor is 735 amino acids long (Figure 30). The full-length PRO545 protein shown in Figure 30 has an estimated molecular weight of about 80,177 daltons and a pI of about 7.08. Important regions of the PRO545 amino acid sequence include the signal peptide, corresponding to amino acids 1-28, five potential N-glycosylation sites, from about amino acid 111-114, amino acids 146-149, amino acids 348-351, amino acids 449-452, and amino acids 648-651, and a neutral zinc metalloproteinase, zinc-binding region signature sequence, from about amino acids 344-353. Clone UNQ346 (DNA49624-1279) has been deposited with ATCC and is assigned ATCC deposit no. 209655.

EXAMPLE 14: Isolation of cDNA Clones Encoding Human PRO617

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42798. Based on the DNA42798 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO617.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-ACGGGCACACTGGATCCCAAATG-3' (SEQ ID NO:86)

reverse PCR primer 5'-GGTAGAGATGTAGAAGGGCAAGCAAGACC-3' (SEQ ID NO:87)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA42798 sequence which had the following nucleotide sequence

hybridization probe

5'-GCTCCCTACCCGTGCAGGTTTCTTCATTGTTCTTAAACAGTATGCCG-3' (SEQ ID NO:88)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO617 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO617 [herein designated as UNQ353 (DNA48309-1280)] (SEQ ID NO:1) and the derived protein sequence for PRO617.

The entire nucleotide sequence of UNQ353 (DNA48309-1280) is shown in Figure 32 (SEQ ID NO:84). Clone UNQ353 (DNA48309-1280) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 723-725 and ending at the stop codon at nucleotide positions 924-926 (Figure 32). The predicted polypeptide precursor is 67 amino acids long (Figure 33). The full-length PRO617 protein shown in Figure 33 has an estimated molecular weight of about 6,981 daltons and a pI of about 7.47. Analysis of the PRO617 amino acid sequence also evidences the existence of a putative signal peptide from about amino acid 15 to about amino acid 27 and a putative protein kinase C phosphorylation site from about amino acid 41 to about amino acid 43. Clone UNQ353 (DNA48309-1280) has been deposited on March 5, 1998 with ATCC and is assigned ATCC deposit no. 209656.

Analysis of the amino acid sequence of the full-length PRO617 polypeptide suggests that it possesses significant homology to the CD24 protein, thereby indicating that PRO617 may be a novel CD24 homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO617 amino acid sequence and the following Dayhoff sequences, CD24_HUMAN, CD24_MOUSE, S15785, CD24_RAT, VGE BPG4, MSE5_HUMAN, HSMHC3W36A_2, MLU15184_8, P R85075, SEPL_HUMAN and MTCY63_13.

EXAMPLE 15: Isolation of cDNA Clones Encoding Human PRO700

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA30837. Based on the DNA30837 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO700.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-ATGTTCTTCGCGCCCTGGTG-3' (SEQ ID NO:91)

forward PCR primer 2 5'-CCAAGCCAACACTCTACAG-3' (SEQ ID NO:92)

reverse PCR primer 1 5'-AAGTGGTCGCCTTGTGCAACGTGC-3' (SEQ ID NO:93)

reverse PCR primer 2 5'-GGTCAAAGGGGATATATGCCAC-3' (SEQ ID NO:94)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30837 sequence which had the following nucleotide sequence

hybridization probe

5'-GCATGGAAGATGCCAAAGTCTATGTGGCTAAAGTGGACTGCACGGCCCA-3'

(SEQ ID NO:95)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO700 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).